



#4

## SEQUENCE LISTING

&lt;110&gt; Autogen Research Pty Ltd

&lt;120&gt; Novel genes and their use in the modulation of obesity, diabetes and energy imbalance

&lt;130&gt; 2309315/TDO

&lt;140&gt; 10/039,050

&lt;141&gt; 2001-12-31

&lt;150&gt; 60/141,441

&lt;151&gt; 1999-06-29

&lt;160&gt; 22

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1669

&lt;212&gt; DNA

&lt;213&gt; mammalian

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (43)..(1104)

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Gly Ile Phe Leu Cys Leu Ile Phe Leu Glu Lys Ser Trp Gly Gln Ile  
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caa atg tcg tgt tgg ccc aag cct ttg att cca gaa ctt gag agg cag 150  
Gln Met Ser Cys Trp Pro Lys Pro Leu Ile Pro Glu Leu Glu Arg Gln  
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aga tgc acc gtt gta aca cca aaa gtc ttc cga gtc gga gaa tat gaa 198  
Arg Cys Thr Val Val Thr Pro Lys Val Phe Arg Val Gly Glu Tyr Glu  
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caa gtt aca ttt gaa gcc cac ggt cac act gac cca ttt gat gta acc	246
Gln Val Thr Phe Glu Ala His Gly His Thr Asp Pro Phe Asp Val Thr	
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atc tct ata aaa agt tac cct gat aaa aat gct aat tac tct tca agc	294
Ile Ser Ile Lys Ser Tyr Pro Asp Lys Asn Ala Asn Tyr Ser Ser Ser	
70 75 80	
tct gta cat tta tca cca gaa aat aaa ttc aaa aac tct aca atc tta	342
Ser Val His Leu Ser Pro Glu Asn Lys Phe Lys Asn Ser Thr Ile Leu	
85 90 95 100	
aca att cag ccc aaa cag ttg tct gaa ggg caa aac tcg tct tcg cat	390
Thr Ile Gln Pro Lys Gln Leu Ser Glu Gly Gln Asn Ser Ser Ser His	
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gtg tat ttg gaa gtt gtg tcc aag cat ttt tca aca tca aaa ata atg	438
Val Tyr Leu Glu Val Val Ser Lys His Phe Ser Thr Ser Lys Ile Met	
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tca atc gtc tat gac aat ggc act ctc ttc att cag act gac aag cct	486
Ser Ile Val Tyr Asp Asn Gly Thr Leu Phe Ile Gln Thr Asp Lys Pro	
135 140 145	
gtg tac act cca gag cag cct gta aag gtt gcc gtg tat tcg ctg gat	534
Val Tyr Thr Pro Glu Gln Pro Val Lys Val Ala Val Tyr Ser Leu Asp	
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Glu Ala Leu Lys Pro Val Thr Arg Glu Thr Val Leu Thr Phe Ile Asp	
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cct gaa gga tcc gaa gtt ggc ata gta gaa gga agc aat cat act gga	630
Pro Glu Gly Ser Glu Val Gly Ile Val Glu Gly Ser Asn His Thr Gly	
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Ile Thr Ser Phe Pro Asp Phe Arg Ile Pro Thr Asn Pro Lys Pro Gly	
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Arg Trp Met Ile Lys Ala Lys Tyr Arg Glu Asp Ala Ser Thr Ala Gly	
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acc aca cac ttt gaa att aaa gag cat gat aaa gct ttc aaa ata gcc	774
Thr Thr His Phe Glu Ile Lys Glu His Asp Lys Ala Phe Lys Ile Ala	
230 235 240	
ctc gtt cca aca agt gat ctg gaa cac cca atg gaa gaa gca cgt ggc	822
Leu Val Pro Thr Ser Asp Leu Glu His Pro Met Glu Glu Ala Arg Gly	
245 250 255 260	
ctg agt ctc cag cca aaa aag tcc ctg caa gag atg ata cat gag caa	870
Leu Ser Leu Gln Pro Lys Lys Ser Leu Gln Glu Met Ile His Glu Gln	
265 270 275	
gct tcg aaa tac aaa cat cca gta ctg aag aaa tgt tgt tat gat gga	918

Ala Ser Lys Tyr Lys His Pro Val Leu Lys Lys Cys Cys Tyr Asp Gly  
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gcc aga tat aac cac cat gaa acc tgt gag gaa cga gtt gcc cgt gtg 966  
Ala Arg Tyr Asn His His Glu Thr Cys Glu Glu Arg Val Ala Arg Val  
295 300 305

aaa ata ggc cca aac tgt gtc aga gcc ttc agt gaa tgc tgt gcc ctg 1014  
Lys Ile Gly Pro Asn Cys Val Arg Ala Phe Ser Glu Cys Cys Ala Leu  
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Ala Ser Glu Asn Thr Phe Lys Asn Ile Leu Met Ser Arg Pro Asp Asp  
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345 350

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Leu Glu Arg Gln Arg Cys Thr Val Val Thr Pro Lys Val Phe Arg Val  
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Gly Glu Tyr Glu Gln Val Thr Phe Glu Ala His Gly His Thr Asp Pro  
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Phe Asp Val Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Asn Ala Asn  
 65 70 75 80  
 Tyr Ser Ser Ser Ser Val His Leu Ser Pro Glu Asn Lys Phe Lys Asn  
 85 90 95  
 Ser Thr Ile Leu Thr Ile Gln Pro Lys Gln Leu Ser Glu Gly Gln Asn  
 100 105 110  
 Ser Ser Ser His Val Tyr Leu Glu Val Val Ser Lys His Phe Ser Thr  
 115 120 125  
 Ser Lys Ile Met Ser Ile Val Tyr Asp Asn Gly Thr Leu Phe Ile Gln  
 130 135 140  
 Thr Asp Lys Pro Val Tyr Thr Pro Glu Gln Pro Val Lys Val Ala Val  
 145 150 155 160  
 Tyr Ser Leu Asp Glu Ala Leu Lys Pro Val Thr Arg Glu Thr Val Leu  
 165 170 175  
 Thr Phe Ile Asp Pro Glu Gly Ser Glu Val Gly Ile Val Glu Gly Ser  
 180 185 190  
 Asn His Thr Gly Ile Thr Ser Phe Pro Asp Phe Arg Ile Pro Thr Asn  
 195 200 205  
 Pro Lys Pro Gly Arg Trp Met Ile Lys Ala Lys Tyr Arg Glu Asp Ala  
 210 215 220  
 Ser Thr Ala Gly Thr Thr His Phe Glu Ile Lys Glu His Asp Lys Ala  
 225 230 235 240  
 Phe Lys Ile Ala Leu Val Pro Thr Ser Asp Leu Glu His Pro Met Glu  
 245 250 255  
 Glu Ala Arg Gly Leu Ser Leu Gln Pro Lys Lys Ser Leu Gln Glu Met  
 260 265 270  
 Ile His Glu Gln Ala Ser Lys Tyr Lys His Pro Val Leu Lys Lys Cys  
 275 280 285  
 Cys Tyr Asp Gly Ala Arg Tyr Asn His His Glu Thr Cys Glu Glu Arg  
 290 295 300  
 Val Ala Arg Val Lys Ile Gly Pro Asn Cys Val Arg Ala Phe Ser Glu  
 305 310 315 320  
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Pro Ala Leu Glu Thr Glu Gly Leu Arg Phe Leu His Val Thr Val Gly	
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Ser Leu Leu Ala Ser Tyr Gly Trp Tyr Val Leu Phe Ser Cys Ile Leu	
30 35 40	
ctc tac att gtc atc cag aag ctc tcc gtc cga ttg agg gtt ttg agg	196
Leu Tyr Ile Val Ile Gln Lys Leu Ser Val Arg Leu Arg Val Leu Arg	
45 50 55	
cag agg cag ctg gac cag gct gac gct gtt ctg gaa cct gat gct gtt	244
Gln Arg Gln Leu Asp Gln Ala Asp Ala Val Leu Glu Pro Asp Ala Val	
60 65 70 75	
gtt aag cga caa gag gct tta gcc gct gct cgt ttg aga atg cag gaa	292
Val Lys Arg Gln Glu Ala Leu Ala Ala Arg Leu Arg Met Gln Glu	
80 85 90	
gat cta aat gcc caa gtt gaa aag cat aag gaa aaa cta aga cag ctt	340
Asp Leu Asn Ala Gln Val Glu Lys His Lys Glu Lys Leu Arg Gln Leu	
95 100 105	
gaa gaa gaa aaa agg aga cag aag att gaa atg tgg gac agc atg caa	388
Glu Glu Glu Lys Arg Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln	
110 115 120	
gaa ggc aga agt tac aga aga aat cca gga agg cct cag gaa gaa gat	436
Glu Gly Arg Ser Tyr Arg Arg Asn Pro Gly Arg Pro Gln Glu Glu Asp	
125 130 135	
ggg cct gga cct tct act tca tca tct gtc acc cgc aaa gga aaa tct	484
Gly Pro Gly Pro Ser Thr Ser Ser Ser Val Thr Arg Lys Gly Lys Ser	
140 145 150 155	
gac aaa aag cct ttg agg gga aat ggt tat aac cct ctg acg ggt gaa	532
Asp Lys Lys Pro Leu Arg Gly Asn Gly Tyr Asn Pro Leu Thr Gly Glu	
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gaggtggggc ttatttccat tcgtagctac ctgtattcta agggctttgg tcagtgtgag 749

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<213> mammalian

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 35 40 45

Gln Lys Leu Ser Val Arg Leu Arg Val Leu Arg Gln Arg Gln Leu Asp  
 50 55 60

Gln Ala Asp Ala Val Leu Glu Pro Asp Ala Val Val Lys Arg Gln Glu  
 65 70 75 80

Ala Leu Ala Ala Ala Arg Leu Arg Met Gln Glu Asp Leu Asn Ala Gln  
 85 90 95

Val Glu Lys His Lys Glu Lys Leu Arg Gln Leu Glu Glu Glu Lys Arg  
 100 105 110

Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln Glu Gly Arg Ser Tyr  
 115 120 125

Arg Arg Asn Pro Gly Arg Pro Gln Glu Glu Asp Gly Pro Gly Pro Ser  
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Thr Ser Ser Ser Val Thr Arg Lys Gly Lys Ser Asp Lys Lys Pro Leu  
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 Ser Ala Arg Pro Ala Leu Glu Thr Glu Gly Leu Arg Phe Leu His Thr  
 10 15 20

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 Thr Val Gly Ser Leu Leu Ala Thr Tyr Gly Trp Tyr Ile Val Phe Ser  
 25 30 35 40

tgc atc ctt ctg tac gtg gtc ttt cag aag ctt tcc gcc cgg cta aga 198  
 Cys Ile Leu Leu Tyr Val Val Phe Gln Lys Leu Ser Ala Arg Leu Arg  
 45 50 55

gcc ttg agg cag agg cag ctg gac cga gct gcg gct gct gtg gaa cct 246  
 Ala Leu Arg Gln Arg Gln Leu Asp Arg Ala Ala Ala Val Glu Pro  
 60 65 70

gat gtt gtt gtt aaa cga caa gaa gct tta gca gct gct cga ctg aaa 294  
 Asp Val Val Val Lys Arg Gln Glu Ala Leu Ala Ala Ala Arg Leu Lys  
 75 80 85

atg caa gaa gaa cta aat gcg caa gtt gaa aag cat aag gaa aaa ctg 342  
 Met Gln Glu Glu Leu Asn Ala Gln Val Glu Lys His Lys Glu Lys Leu  
 90 95 100

aaa caa ctt gaa gaa gaa aaa agg aga cag aag att gaa atg tgg gac 390  
 Lys Gln Leu Glu Glu Glu Lys Arg Arg Gln Lys Ile Glu Met Trp Asp  
 105 110 115 120

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 Ser Met Gln Glu Gly Lys Ser Tyr Lys Gly Asn Ala Lys Lys Pro Gln  
 125 130 135

gag gaa gac agt cct ggg cct tcc act tca tct gtc ctg aaa cgg aaa 486  
 Glu Glu Asp Ser Pro Gly Pro Ser Thr Ser Ser Val Leu Lys Arg Lys  
 140 145 150

tcg gac aga aag cct ttg cgg gga gga ggt tat aac ccg ttg tct ggt 534  
 Ser Asp Arg Lys Pro Leu Arg Gly Gly Gly Tyr Asn Pro Leu Ser Gly  
 155 160 165

gaa gga ggc gga gct tgc tcc tgg aga cct gga cgc aga ggc ccg tca 582  
 Glu Gly Gly Gly Ala Cys Ser Trp Arg Pro Gly Arg Arg Gly Pro Ser  
 170 175 180

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 Ser Gly Gly  
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Tyr Gly Trp Tyr Ile Val Phe Ser Cys Ile Leu Leu Tyr Val Val Phe  
 35 40 45

Gln Lys Leu Ser Ala Arg Leu Arg Ala Leu Arg Gln Arg Gln Leu Asp  
 50 55 60



Arg Ala Ala Ala Ala Val Glu Pro Asp Val Val Val Lys Arg Gln Glu  
65 70 75 80

Ala Leu Ala Ala Ala Arg Leu Lys Met Gln Glu Glu Leu Asn Ala Gln  
85 90 95

Val Glu Lys His Lys Glu Lys Leu Lys Gln Leu Glu Glu Glu Lys Arg  
100 105 110

Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln Glu Gly Lys Ser Tyr  
115 120 125

Lys Gly Asn Ala Lys Lys Pro Gln Glu Glu Asp Ser Pro Gly Pro Ser  
130 135 140

Thr Ser Ser Val Leu Lys Arg Lys Ser Asp Arg Lys Pro Leu Arg Gly  
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Leu Ser Pro His Ser Val Ala Ser Met Leu Ser Ala Val Glu Ala Gly  
5 10 15

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Thr Val Phe Leu Leu Val Thr Ser Leu Pro His  
20 25

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